Methanol Expression Regulator 1 (Mxr1p) is Essential for the Utilization of Amino Acids as the Sole Source of Carbon by the Methylotrophic Yeast, *Pichia pastoris*

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Supplemental data

Identification of proteins bands a-f in Fig 1C by mass spectrometry. Protein bands of interest were excised precisely from the Coomassie blue-stained SDS polyacrylamide gel and subjected to in-gel trypsin digestion using Trypsin profile IGD kit (SigmaAldrich). MALDI TOF was performed in HCT Ultra PTM Discovery System (ETD II- Bruker Daltonics) with 1100 series HPLC (Agilent). For identification of proteins, obtained 'peak list' was searched against NCBI non redundant database using MASCOT protein mass fingerprint software.

Summary of MASCOT search results

1. Identification of protein (a) as *P. pastoris/Komagataella phaffii* Glutamate dehydrogenase 2:

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Taxonomy : Other Fungi (5444939 sequences)
Timestamp : 14 Jun 2016 at 17:51:49 GMT
Warning : Specifying a protein mass disables query intensity in PMF-search
Warning : Specifying a protein mass disables mixture mode in PMF-search
Top Score : 66 for gi|254568192, NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate [Komagataella phaffii GS115]

601.460	2261	2356.44	969
604.208	2773	4565.62	1718
606.185	2315	11315.25	4891
607.354	849	1757.87	1896
616.459	2536	1461.36	525
628.229	1900	3870.56	2046
629.435	1263	4643.34	3655
634.277	2421	4107.12	1702
642.319	2060	4085.05	1911
644.223	2133	23841.48	11476
650.247	2308	30583.63	13628
656.260	2490	13032.60	5327
666.229	2329	37379.88	17055
668.262	2032	3563.70	1910

672.237	2482	18085.34	7811
682.215	2355	23647.89	10844
684.228	2346	2761.87	1284
685.577	2151	4351.71	2413
688.211	2308	9439.48	4847
704.193	2609	3374.32	1590
706.581	2001	2804.63	2100
707.624	2243	2162.89	923
708.541	2001	1901.68	1069
710.459	1764	1102.78	674
720.666	2119	3215.91	1744
722.646	2110	4483.87	3273
723.583	2285	1802.76	913
724.521	2277	1547.04	734
728.580	2238	1152.32	562
744.616	2275	3475.47	1865
760.647	2281	1662.85	915
766.628	2209	1695.01	973
781.656	3148	1034.79	535
782.613	2311	3386.97	1922
785.658	2357	691.15	444
813.657	2852	910.81	421
825.447	2205	1288.75	826
839.353	2342	935.67	595
841.355	2987	2015.29	1006
845.387	2595	2939.57	1672
855.326	2372	5688.60	3615
857.324	2713	1808.93	1097
861.364	2499	17164.97	10436
871.316	2433	6544.52	4382
877.351	2459	23005.18	14692
879.334	1292	1688.45	2422
893.329	2399	13444.76	9358
895.314	1638	1873.24	1988
899.307	2719	738.27	499
909.297	2367	4770.51	3368
911.399	1383	802.29	920
915.285	1472	512.33	613
936.749	1918	884.75	868
953.727	2328	446.82	358
958.735	2794	473.65	309
974.784	2552	744.18	506
975.789	2191	775.44	621
991.789	2656	774.59	567
1000.856	2134	895.09	819
1021.837	1935	789.92	921
1050.452	2350	645.02	610
1060.423	1966	1321.10	1403
1066.413	2251	2508.04	2484
1072.413	2596	836.11	621
1082.391	2439	2768.74	2531
1088.364	2732	1417.28	1234
1098.373	2895	1594.88	1233
1104.331	2065	899.72	1125
1214.067	2643	315.11	309
1223.030	2304	283.53	338
1230.994	2182	351.75	435
1236.092	2443	662.48	723
1252.058	2688	642.14	656
1277.441	2871	470.36	479

1289.052	2358	585.53	718
1293.438	3424	610.28	592
1304.010	3096	501.68	500
1309.414	2068	252.81	433
1318.992	2779	266.31	284
1379.107	1886	539.44	940
1401.017	1412	188.28	404
1416.989	2999	221.49	256
1504.369	2797	141.57	209
1564.268	2670	314.74	533
1586.266	3568	127.44	154
1588.234	3049	238.95	328
1610.264	2831	265.07	408
1623.201	2601	206.36	399
1626.233	2888	434.82	680
1656.357	3029	180.72	255
1671.898	989	73.39	327
1730.278	2390	119.78	256
1839.314	3105	136.39	269
1854.368	3453	94.91	160
1877.362	3514	268.60	455
1881.371	2841	1220.29	2578
1957.234	3514	187.75	330
2148.486	2879	67.24	167
2272.749	2706	81.32	296
2288.577	3037	116.85	346

Concise Protein Summary Report

1. gi|254568192 **Mass:** 117627 **Score:** 66 **Expect:** 1.5 **Matches:** 29
NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate [Komagataella phaffii GS115]

2. gi|1027026648 **Mass:** 67285 **Score:** 66 **Expect:** 1.5 **Matches:** 19
hypothetical protein Z520_07198 [Fonsecaea multimorphosa CBS 102226]

3. gi|808362097 **Mass:** 16409 **Score:** 50 **Expect:** 54 **Matches:** 10
3-ketoacyl-CoA thiolase [Pseudozyma hubeiensis SY62]

4. gi|648171492 **Mass:** 56234 **Score:** 50 **Expect:** 58 **Matches:** 17
hypothetical protein GALMADRAFT_52566 [Galerina marginata CBS 339.88]

5. gi|1027188691 **Mass:** 101224 **Score:** 49 **Expect:** 73 **Matches:** 23
hypothetical protein NEIG_01641 [Nematocida sp. ERTm5]

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : 117 kDa
Peptide Mass Tolerance : ± 0.5 Da

Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 100

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2. Identification of protein (b) as *P. pastoris/Komagataella phaffii* Alcohol oxidase 1:

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Taxonomy : Other Fungi (5444939 sequences)
Timestamp : 14 Jun 2016 at 17:59:35 GMT
Warning : Specifying a protein mass disables query intensity in PMF-search
Warning : Specifying a protein mass disables mixture mode in PMF-search
Top Score : 88 for gi|254574324, Alcohol oxidase [Komagataella phaffii GS115]

604.209	2751	4277.18	1834
606.175	2466	17778.44	6871
614.274	1891	6370.72	3042
622.174	2620	3429.63	1300
628.204	2273	7051.06	3081
630.203	2309	13812.85	5915
632.194	2328	2255.20	910
634.319	1491	2861.12	1659
642.328	2104	4860.01	2173
644.225	2136	36535.97	17385
650.262	2052	21814.94	10603
656.294	2301	2672.39	1115
659.223	2382	2589.85	1111
660.255	2180	3111.39	1412
666.237	2128	25602.79	12776
668.271	2168	3563.78	1763
672.263	2232	4563.27	2068
682.219	2143	13478.24	6714
684.264	2263	1888.02	926
688.233	2262	2453.19	1133
704.215	2234	1038.58	540
706.218	2189	1029.35	556
801.650	2113	1109.58	897
804.552	1793	604.74	477
819.405	1832	3176.07	2563
825.407	2231	3297.03	2050
833.280	2805	1206.51	686
841.349	2280	6741.33	4471
845.431	2066	955.19	655
855.319	2454	11194.22	6965
857.312	2418	7103.70	4455
861.379	2275	7895.93	5142
871.304	2536	9269.09	5678
877.356	2252	10077.09	7002
879.328	1900	1493.34	1189
893.324	2288	5607.07	4045
895.269	2354	1918.46	1305
909.283	2302	1473.56	1084
925.731	2128	1965.47	1731

939.751	2517	7603.43	5408
1010.813	2441	726.24	608
1030.393	2672	1095.77	899
1044.353	2106	514.81	513
1046.359	2664	1880.50	1455
1050.406	2438	723.41	595
1060.362	2692	3291.77	2518
1066.389	2631	3850.67	3113
1080.898	2731	598.93	454
1082.362	2470	3672.79	3125
1084.329	3247	809.16	491
1088.348	3510	977.59	594
1098.339	2804	1780.96	1352
1118.805	2262	437.29	469
1143.943	2493	344.29	393
1183.978	2680	5480.34	5141
1217.948	3831	563.04	417
1221.914	3172	621.59	514
1227.942	3160	588.93	488
1230.005	3140	944.49	858
1271.348	3583	594.64	460
1277.392	2926	792.84	842
1287.287	2794	284.42	379
1293.360	2579	912.40	1118
1309.305	3048	388.58	396
1315.132	3104	430.05	415
1353.972	2828	875.77	1032
1383.060	3483	351.70	347
1446.017	3310	4396.15	4692
1448.225	3049	10158.61	11807
1459.161	3457	1829.78	1942
1472.079	3239	1516.94	1707
1482.220	3334	534.08	615
1486.206	3986	293.44	282
1510.074	2714	244.63	344
1523.157	3516	477.59	495
1524.126	3420	993.94	1129
1582.221	3268	401.18	540
1596.239	2653	298.24	495
1602.115	3782	1448.35	1652
1644.188	3553	6390.64	8202
1676.100	4127	1174.01	1354
1682.211	3069	289.29	480
1711.148	4467	231.56	266
1750.208	3754	3731.35	4974
1795.147	3731	1212.83	1798
1885.443	3227	575.84	1096
1895.331	4810	239.74	368
1941.312	3015	117.34	218
1980.314	3851	1243.75	2071
2013.505	3589	198.49	349
2026.287	3853	894.95	1533
2170.353	4189	331.16	533
2319.535	3882	339.65	695
2412.476	4760	1292.35	2222
2515.501	4376	263.04	510
2603.607	2490	145.93	313
2671.581	4903	152.77	326
2698.783	4940	319.61	682
2749.589	5203	355.01	691

3672.074	6480	233.63	573

Concise Protein Summary Report

1. gi|254574324 **Mass:** 73851 **Score: 88** **Expect:** 0.009 **Matches:** 19
   Alcohol oxidase [Komagataella phaffii GS115]
   gi|37694459 **Mass:** 73865 **Score: 88** **Expect:** 0.009 **Matches:** 19
   alcohol oxidase AOX1 [Ogataea pini]

2. gi|2104963 **Mass:** 73878 **Score:** 62 **Expect:** 3.2 **Matches:** 16
   alcohol oxidase [Komagataella pastoris]
   gi|254572894 **Mass:** 73905 **Score:** 62 **Expect:** 3.2 **Matches:** 16
   hypothetical protein [Komagataella phaffii GS115]

3. gi|1027143329 **Mass:** 17053 **Score:** 56 **Expect:** 14 **Matches:** 9
   hypothetical protein CC84DRAFT_866443 [Paraphaeosphaeria sporulosa]

4. gi|302511255 **Mass:** 48315 **Score:** 56 **Expect:** 15 **Matches:** 17
   hypothetical protein ARB_04461 [Arthroderma benhamiae CBS 112371]

5. gi|158251748 **Mass:** 34114 **Score:** 53 **Expect:** 29 **Matches:** 14
   hypothetical protein [Pleurotus ostreatus]

Search Parameters

Type of search : Peptide Mass Fingerprint

Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : 70 kDa
Peptide Mass Tolerance : ± 0.5 Da
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 100

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3. Identification of protein (c) as *P. pastoris/Komagataella phaffii* Formate dehydrogenase:

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Taxonomy : Other Fungi (5444939 sequences)
Timestamp : 14 Jun 2016 at 18:05:39 GMT
Warning : Specifying a protein mass disables query intensity in PMF-search
Warning : Specifying a protein mass disables mixture mode in PMF-search
Top Score : 60 for gi|25452123, NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate [Komagataella phaffii GS115]

586.364	1918	1644.05	770

606.148	1734	3271.12	2050
634.456	1663	3160.73	1968
644.184	1721	3220.59	2043
666.120	1609	3007.87	2358
668.410	1611	1727.91	1241
682.119	2036	2614.57	1561
710.495	2174	14121.38	7747
728.500	1729	1492.78	1132
748.456	2254	2906.15	1667
767.502	2109	1693.44	1106
786.490	2043	1427.53	972
788.557	1854	2054.40	1674
804.516	1635	3963.79	3848
805.588	3193	2183.92	927
826.586	1848	2657.30	2132
828.692	1792	2568.69	2175
842.581	1588	2452.45	2509
859.696	2053	4547.18	3528
881.616	1986	866.62	444
893.191	2643	780.00	366
909.182	2923	434.22	177
938.594	2710	648.67	249
948.582	2222	661.81	292
976.633	2077	598.23	255
987.757	2288	9016.84	7714
1009.707	2382	767.49	352
1025.688	2295	1229.90	1136
1033.745	2772	707.06	339
1049.768	2608	735.29	311
1072.721	2293	843.95	474
1087.761	2463	649.46	341
1110.682	2581	945.47	489
1148.680	2583	930.29	436
1165.799	2779	640.01	295
1181.744	2865	616.41	310
1204.863	2566	9224.75	9533
1210.864	2378	2717.12	3159
1226.852	2930	909.46	417
1232.864	3489	431.59	225
1242.789	2642	2106.16	2238
1248.791	2862	794.36	389
1264.816	3301	476.78	228
1280.768	3410	492.53	198
1306.915	4174	326.22	140
1335.936	2101	983.07	1524
1370.949	2949	583.35	301
1401.136	2333	415.53	302
1408.913	3153	430.19	259
1423.118	1964	455.81	340
1450.998	3061	1161.24	688
1485.003	4073	500.70	239

1501.897	2676	901.15	1492
1518.880	2644	1069.90	1845
1540.977	2496	1795.08	2860
1556.933	2457	2134.12	4138
1578.937	3384	767.14	438
1639.561	3365	413.00	235
1679.092	2598	836.03	1610
1762.959	4627	369.91	174
1807.180	2830	979.74	1936
1880.140	4233	627.06	387
1947.293	4955	417.65	256
2235.274	4340	1064.77	722
2257.341	3284	607.46	1392
2273.299	3514	1110.37	2576
2316.306	3202	550.30	1446
2354.380	3196	700.04	1894
2539.353	5705	302.82	201
2705.875	4832	212.52	140
2733.547	4600	350.09	319

Concise Protein Summary Report

1. gi|254572123 **Mass:** 40285 **Score:** 60 **Expect:** 5.2 **Matches:** 18
   NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate [Komagataella phaffii GS115]

2. gi|1026948073 Mass: 71347 Score: 59 Expect: 4.9 Matches: 17
   hypothetical protein SPPG_00158 [Spizellomyces punctatus DAOM BR117]

3. gi|1032873058 Mass: 43421 Score: 59 Expect: 3.5 Matches: 21
   26S protease regulatory subunit 8 [Purpureocillium lilacinum]

4. gi|591490653 Mass: 38793 Score: 59 Expect: 6.3 Matches: 20
   succinyl-CoA synthetase beta subunit [Fusarium oxysporum f. sp. vasinfectum 25433]

5. *gi|818155629 Mass: 53490 Score: 53 Expect: 29 Matches: 18*
   26S protease regulatory subunit 8 [Trichoderma harzianum]

Type of search : Peptide Mass Fingerprint

Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : 40 kDa
Peptide Mass Tolerance : ± 1.2 Da
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 71

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4. Identification of protein (d) as *P. pastoris/Komagataella phaffii* Aconitase 1:

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Timestamp : 14 Jun 2016 at 18:31:49 GMT
Warning : Specifying a protein mass disables query intensity in PMF-search
Warning : Specifying a protein mass disables mixture mode in PMF-search
Top Score : 143 for gi|254564667, Aconitase, required for the tricarboxylic acid (TCA) cycle [Komagataella phaffii GS115]

602.839	3041	68.98	24
624.804	3190	133.51	44
666.917	2804	439.89	161
692.933	3938	108.47	32
697.095	2497	173.24	75
709.664	3905	51.42	17
715.990	2377	315.26	151
835.161	2477	150.61	86
872.166	2977	334.94	181
881.153	2357	213.32	139
921.140	3184	264.71	141
923.196	2681	223.56	141
937.297	3659	54.09	25
972.232	4890	63.59	24
983.354	2655	59.95	40
1009.359	2304	317.22	262
1038.343	2872	407.78	294
1044.223	2825	66.29	51
1076.423	4038	78.60	41
1083.478	2947	436.25	321
1090.426	2913	144.65	118
1148.570	2580	968.85	898
1158.575	3076	91.27	74
1168.555	2667	107.52	112
1171.545	3586	144.17	99
1179.482	4262	92.19	50
1189.498	3103	695.27	579
1210.511	5031	73.29	41
1230.699	2434	76.90	79
1239.578	2952	349.93	319
1250.519	3176	99.61	91
1291.612	2993	306.03	309
1318.628	5316	92.56	55
1346.691	3017	390.60	433
1369.679	3275	605.28	603
1451.781	2844	1364.94	1721
1470.764	3430	701.24	806
1473.771	3693	134.58	136
1507.854	3868	91.93	105
1515.742	4496	97.79	105
1558.816	3524	1210.29	1421
1594.855	3491	2819.39	1408
1604.884	3149	88.23	134
1641.868	4511	160.36	183

1660.921	3251	1265.48	1835
1730.004	3535	1951.08	2924
1746.019	5394	160.45	154
1765.040	3659	785.97	1144
1775.055	3214	380.39	686
1779.988	4477	125.40	152
1792.062	3512	1321.03	2148
1809.961	3186	1993.09	3621
1905.066	3146	765.79	1576
1920.152	4490	141.27	187
1928.154	3847	117.32	178
1943.125	3233	1722.97	3462
1951.240	3945	93.52	144
1964.236	3426	2495.53	4901
2024.326	3540	1424.07	2644
2093.260	3740	96.70	178
2169.499	3421	1080.16	2375
2194.484	4309	76.09	163
2411.043	2753	54.67	198
2414.479	3070	200.46	662
2550.411	3042	35.98	101
2558.614	4117	126.52	328
2787.756	4217	151.76	305
2789.796	3984	753.64	1932
3106.218	2855	35.65	134
3142.065	4047	336.29	1197

Concise Protein Summary Report

1. gi|254564667 **Mass:** 84496 **Score: 143** **Expect:** 4.4e-07 **Matches:** 33

Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitoc [Komagataella phaffii GS115]

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2. gi|953490580 **Mass:** 39589 **Score:** 72 **Expect:** 5 **Matches:** 17
Protein phosphatase 1, regulatory subunit, and related proteins [Plasmopara halstedii]

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3. gi|1022630977 **Mass:** 161946 **Score:** 71 **Expect:** 7.5 **Matches:** 24
hypothetical protein PV10_04424 [Exophiala mesophila]

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4. gi|516126108 **Mass:** 15022 **Score:** 70 **Expect:** 8.1 **Matches:** 11
hypothetical protein [Nocardiopsis baichengensis]

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5. gi|757183878 **Mass:** 59061 **Score:** 70 **Expect:** 8.6 **Matches:** 22
hypothetical protein [Lachnospiraceae bacterium TWA4]

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : 75 kDa
Peptide Mass Tolerance : ± 1.2 Da

Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 70

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5. Identification of protein (e) as *P. pastoris/Komagataella phaffii* Malate synthase 1:

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Timestamp : 15 Jun 2016 at 05:13:27 GMT
Warning : Specifying a protein mass disables query intensity in PMF-search
Warning : Specifying a protein mass disables mixture mode in PMF-search
Top Score : 89 for gi|254572972, Malate synthase [Komagataella phaffii GS115]

646.805	3334	135.36	43
655.616	2986	119.29	41
664.821	3449	150.55	45
687.832	3074	112.40	44
698.562	4241	103.52	28
699.628	3962	130.25	34
714.990	2455	214.90	93
725.919	4076	134.07	39
742.980	3324	102.11	37
751.053	2517	969.99	488
763.046	2581	1856.06	916
774.171	2245	251.15	159
775.161	2479	406.23	219
802.099	3180	87.71	38
805.025	4263	96.38	36
843.192	2972	229.48	114
850.165	2796	141.77	77
884.321	2067	2654.68	1960
891.231	2327	86.17	65
898.243	2748	327.30	197
902.461	2628	209.36	134
916.191	3099	110.79	59
920.318	2574	151.48	99
925.216	2300	245.26	221
926.297	2270	251.61	191
942.295	3657	179.62	86
949.344	2269	1519.40	1115
970.359	2419	428.75	330
994.383	4145	98.35	46
1004.529	2637	161.31	116
1013.359	2957	136.08	77
1021.532	1991	1073.96	1079
1042.365	2336	293.83	261
1044.568	2208	1707.63	1540
1048.420	2183	327.28	316
1054.467	2835	159.98	121
1099.470	2301	1234.94	1330
1101.488	2499	277.32	222
1112.519	2490	103.37	100

1126.600	2210	1195.53	1246
1136.541	2263	245.41	258
1148.564	3322	130.44	97
1155.575	3281	156.37	112
1160.545	2419	219.89	229
1163.675	2274	2649.82	2773
1189.553	3245	232.45	186
1191.582	2226	1622.30	1900
1200.640	2948	358.73	320
1203.587	2685	1222.12	1209
1207.776	2136	1709.82	2063
1266.625	3963	122.31	90
1284.817	2143	525.89	713
1300.384	838	88.86	299
1306.688	2557	897.82	1093
1347.735	2112	255.20	360
1381.620	2416	250.37	335
1415.824	2593	1978.70	2642
1435.824	2110	131.80	236
1454.861	3740	103.88	101
1471.811	3192	105.23	155
1484.851	3402	125.00	170
1511.891	3696	103.37	104
1514.866	3223	95.68	125
1528.928	2772	329.33	444
1549.991	3286	137.86	183
1635.910	2777	100.81	174
1660.993	2260	140.85	284
1708.067	2797	236.73	503
1725.096	2346	634.87	1614
1825.685	1382	121.85	728
1840.959	2157	96.07	251
1864.374	2221	88.22	248
1902.313	1614	94.14	367
1943.305	2951	1230.50	2796
1962.449	2059	179.59	600
2040.394	2943	201.72	540
2047.348	2801	617.15	1624
2061.608	5674	100.14	243
2084.700	1211	64.13	286
2134.756	2438	48.44	186
2141.397	5304	48.31	72
2472.644	3714	40.33	99
2568.712	3784	46.73	139
2700.847	4903	50.84	27
2770.977	3565	49.36	154

Concise Protein Summary Report

1. gi|254572972 **Mass:** 65590 **Score:** 89 **Expect:** 0.1 **Matches:** 35
   Malate synthase [Komagataella phaffii GS115]
   gi|328354576 **Mass:** 63064 **Score:** 88 **Expect:** 0.13 **Matches:** 35
   malate synthase [Komagataella phaffii CBS 7435]

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2. gi|392716072 **Mass:** 28022 **Score:** 70 **Expect:** 9.9 **Matches:** 21
   GntR family transcriptional regulator [Ralstonia sp. PBA]

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3. gi|729795642 **Mass:** 6397 **Score:** 68 **Expect:** 15 **Matches:** 8
hypothetical protein PU73_23670 [Escherichia coli]

4. gi|922997944 **Mass:** 28127 **Score:** 67 **Expect:** 17 **Matches:** 17
enoyl-CoA hydratase [Bacillus koreensis]

5. gi|516078742 **Mass:** 19173 **Score:** 67 **Expect:** 17 **Matches:** 14
hypothetical protein [beta proteobacterium L13]

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : 65 kDa
Peptide Mass Tolerance : ± 1.2 Da
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 85

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6. Identification of protein (f) as *P. pastoris/Komagataella phaffii* citrate synthase 1

User : umakant
Email : uksahucbt@gmail.com
Database : NCBInr 20160604 (88499796 sequences; 32486953934 residues)
Taxonomy : Other Fungi (5444939 sequences)
Timestamp : 14 Jun 2016 at 18:12:56 GMT
Top Score : 64 for gi|254565307, hypothetical protein [Komagataella phaffii GS115]*

600.428	11.8	153	1951	799.13	354
602.463	16.9	137	2094	1140.49	500
605.490	12.7	236	2182	857.20	349
607.508	62.0	2816	2385	4187.95	1665
610.428	12.2	200	1941	820.32	342
612.411	15.1	235	2181	1017.73	464
626.445	10.4	142	3511	688.78	218
634.470	19.3	428	1964	1228.26	548
647.534	23.3	1154	2486	1379.28	559
649.507	11.7	279	2040	684.60	317
651.452	8.7	109	2490	503.81	204
669.301	12.6	498	900	647.27	650
684.514	28.6	2503	1465	1373.21	1015
689.523	9.5	74	4814	450.60	127
703.503	12.5	220	2222	550.65	279
705.524	13.0	351	2938	565.11	210
707.489	7.5	97	4574	322.42	80
719.535	6.9	80	3559	280.70	93
756.622	9.0	92	3736	284.71	89
804.600	11.4	262	3445	287.89	116

846.721	7.1	67	3070	159.27	79
848.653	10.0	251	3001	225.08	105
875.584	6.9	81	3118	142.39	81
917.671	7.7	82	5341	134.77	37
984.672	7.3	140	4232	124.26	57
993.726	11.1	212	3902	191.28	91
1003.726	14.1	416	2754	244.67	174
1010.732	61.9	19025	2541	1062.65	835
1023.789	25.6	2035	2814	432.33	294
1033.817	16.2	884	1860	270.20	279
1042.774	27.0	3199	3242	444.48	277
1071.754	69.4	17974	2829	1112.95	846
1097.776	7.7	222	4159	123.15	65
1131.769	36.1	3671	2806	559.08	451
1146.842	19.0	1344	3218	286.84	205
1150.868	6.8	166	5347	102.93	47
1161.889	17.9	1289	3599	262.49	181
1194.854	8.9	79	4793	122.47	74
1203.840	8.1	139	3472	110.85	88
1211.741	9.8	262	1688	131.86	185
1218.846	48.6	5520	2773	644.61	608
1226.924	10.5	353	3320	137.36	116
1260.920	10.5	513	3520	132.69	113
1274.983	20.2	1127	3471	259.88	212
1308.039	256.5	120568	2894	3453.02	3547
1331.923	6.6	68	3787	89.60	74
1364.942	45.4	3184	3158	582.03	574
1377.904	10.6	74	4964	132.85	105
1379.004	18.0	359	2370	225.08	320
1395.947	7.9	115	6046	97.62	57
1400.925	10.8	81	3245	133.05	159
1421.777	9.2	99	2078	114.07	183
1422.922	9.6	75	3008	119.27	142
1434.922	7.2	85	5794	90.22	68
1462.899	9.1	523	2477	116.27	208
1490.952	16.4	1942	4023	215.04	196
1534.905	13.8	304	2657	187.60	275
1558.054	9.8	259	5370	129.44	151
1570.037	7.8	167	3721	101.52	106
1618.007	11.8	215	3889	143.95	210
1619.974	10.3	104	3331	125.13	207
1631.042	11.1	219	3197	135.02	178
1654.035	13.0	561	3466	158.93	218
1690.044	7.9	120	4347	99.20	97
1697.683	19.2	275	1093	202.29	1087
1706.015	16.3	122	4187	230.09	300
1736.168	292.1	46692	3776	5036.90	6751
1740.187	639.7	357581	3591	11311.90	15769
1752.112	15.6	2013	4415	294.76	346
1791.170	54.4	51645	3946	984.52	1340
1817.130	17.3	261	4201	267.98	370
1836.219	13.8	267	698	185.91	319
1844.191	15.5	1571	3900	198.02	304
1884.051	6.5	107	1427	70.03	187
1887.256	7.5	242	5857	83.57	84
1911.206	20.2	1151	3709	208.99	350
1928.171	6.1	85	4579	60.15	62
1945.257	17.6	473	3493	146.22	326
1948.051	9.3	157	3939	87.35	132
1954.111	6.5	208	2576	59.43	147

2009.067	8.2	163	3086	57.89	144
2045.213	6.7	107	4342	50.53	90
2050.224	6.1	81	4495	50.01	76
2057.340	10.2	104	4700	83.54	128
2062.317	18.0	425	4106	133.11	276
2066.234	14.7	597	3807	119.77	205
2110.286	11.3	478	4684	89.31	131
2124.246	7.4	258	3964	55.94	93
2167.272	14.1	349	5096	94.93	129
2178.411	23.9	2294	3950	151.98	285
2193.406	6.1	78	5227	38.23	52
2270.255	33.6	1373	4247	177.12	364
2533.468	16.4	563	5030	71.72	130
2550.493	20.4	512	6164	89.77	158
2581.485	13.7	395	5273	54.22	115
2879.146	8.7	83	4510	24.21	55
2931.849	13.0	78	5870	35.46	68
3033.846	7.3	76	941	16.13	59
3089.050	11.5	87	8037	26.86	43
3158.726	11.2	160	4220	25.28	56

Concise Protein Summary Report

1. gi|254565307 **Mass:** 51873 **Score:** 64 **Expect:** 2 **Matches:** 12
hypothetical protein [Komagataella phaffii GS115]

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2. gi|1032903699 **Mass:** 100174 **Score:** 54 **Expect:** 20 **Matches:** 17
hypothetical protein LLEC1_00845 [Cordyceps confragosa]
gi|549048304 **Mass:** 9227 **Score:** 41 **Expect:** 4.7e+02 **Matches:** 3
Protein of unknown function [Pyronema omphalodes CBS 100304]

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3. gi|1023260822 **Mass:** 61173 **Score:** 50 **Expect:** 51 **Matches:** 11
hypothetical protein CALCODRAFT_330062 [Calocera cornea HHB12733]

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4. gi|700491037 **Mass:** 49069 **Score:** 49 **Expect:** 72 **Matches:** 9
O-methyltransferase, family 3 [Penicillium italicum]

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5. gi|953101707 **Mass:** 14422 **Score:** 48 **Expect:** 77 **Matches:** 5
hypothetical protein CNM01675 [Cryptococcus neoformans var. neoformans JEC21]

Search Parameters
Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.5 Da
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 100
Selected for scoring : 20

*** This hypothetical protein has 76% amino acid identity with *Saccharomyces cerevisiae* citrate synthase 1.**